```
                    10              30              50
-88  GTTGCTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT  -29

                    70              90              110
-28  CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGGCCGTCGCTCCACGTCT   31
 -8                                  M  A  W  L  G  A  S  L  H  V  W   11

                    130             150             170
 32  GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGTCTGATGGCA   91
 12   G  W  L  M  L  G  S  C  L  L  A  R  A  Q  L  D  S  D  G  T   31

                    190             210             230
 92  CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGGAAAGTACAATGTGAACTCA  151
 32   I  T  I  E  E  Q  I  V  L  V  L  K  A  K  V  Q  C  E  L  N   51

                    250             270             290
152  ACATCACAGCTCAACTCCAGGAGGGAGAAGGTAATTGTTCCCTGAATGGGATGGACTCA  211
 52   I  T  A  Q  L  Q  E  G  E  G  N  C  F  P  E  W  D  G  L  I   71

                    310             330             350
212  TTTGTTGGCCCAGAGGAACAGTGGGAAAATATCGGCTGTTCCATGCCCTGTCCTTATATT  271
 72   C  W  P  R  G  T  V  G  K  I  S  A  V  P  C  P  P  Y  I  Y   91

                    370             390             410
272  ATGACTTCAACCATAAAGGAGTTGCTTTCCGACACTGTAACCCCAATGGAACATGGGATT  331
 92   D  F  N  H  K  G  V  A  F  R  H  C  N  P  N  G  T  W  D  F  111
```

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

```
              430            450            470
332  TTATGCACAGCTTAAATAAAACATGGGCCAATTATTCAGACTGCCTTCGCTTTCTGCAGC  391
112   M  H  S  L  N  K  T  W  A  N  Y  S  D  C  L  R  F  L  Q  P   131

              490            510            530
392  CAGATATCAGCAGCATAGGAAAGCAAGAATTCTGTGAACGCCTCTATGTAATGTATACCGTTG  451
132   D  I  S  I  G  K  Q  E  F  C  E  R  L  Y  V  M  Y  T  V  G    151

              550            570            590
452  GCTACTCCATCTCTTTGGTTCCTGGCTATTCTCATCATTGGTTACTTCAGAC  511
152   Y  S  I  S  F  G  S  L  A  V  A  I  L  I  I  G  Y  F  R  R   171

              610            630            650
512  GATTGCATTGCACTAGGAACTATATCCACATGCACTTATTGTGTCTTTCATGCTGAGAG  571
172   L  H  C  T  R  N  Y  I  H  M  H  L  F  V  S  F  M  L  R  A   191

              670            690            710
572  CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG  631
192   T  S  I  F  V  K  D  R  V  V  H  A  H  I  G  V  K  E  L  E   211

              730            750            770
632  AGTCCCTAATAATGCAGGATGACCCACAAAATTCCATTGAGGCAACTTCTGTGGACAAAT  691
212   S  L  I  M  Q  D  D  P  Q  N  S  I  E  A  T  S  V  D  K  S   231

              790            810            830
```

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

```
692  CACAATATATCGGGTGCAAGATTGCTGTTGTGATGTTATTACTTCCTGGCTACAAATT      751
232    Q  Y  I  G  C  K  I  A  V  V  M  F  I  Y  F  L  A  T  N  Y    251

752  ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTTCTTT     811
252    Y  W  I  L  V  E  G  L  Y  L  H  N  L  I  F  V  A  F  F  S    271

812  CGGACACCAAATACCTGTGGGCTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTG      871
272    D  T  K  Y  L  W  G  F  I  L  I  G  W  G  F  P  A  A  F  V    291

872  TTGCAGCATGGGCTGTGGCACGAGCAACTCTGGCTGATGCGAGGTGCTGGGAACTTAGTG    931
292    A  A  W  A  V  A  R  A  T  L  A  D  A  R  C  W  E  L  S  A    311

932  CTGGAGACATCAAGTGGATTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA    991
312    G  D  I  K  W  I  Y  Q  A  P  I  L  A  A  I  G  L  N  F  I    331

992  TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG   1051
332    L  F  L  N  T  V  R  V  L  A  T  K  I  W  E  T  N  A  V  G    351

1052 GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCCTGGTCCTAG   1111
352    H  D  T  R  K  Q  Y  R  K  L  A  K  S  T  L  V  L  V  L  V    371
```

MATCH WITH FIG. 1D

FIG.1C

```
                    1210              1230              1250
1112 TCTTTGGAGTGCATTACATCGTTGTTCGTGTGCTGCCTCACTCCTTCACTGGGCTCGGGT 1171
 372   F   G   V   H   Y   I   V   F   V   C   L   P   H   S   F   T   G   L   G   W   391

                    1270              1290              1310
1172 GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTCAGGGTTTCTTTGTGTCTA 1231
 392   E   I   R   M   H   C   E   L   F   F   N   S   F   Q   G   F   F   V   S   I   411

                    1330              1350              1370
1232 TCATCTACTGCTACTGCAATGGGAGAGGTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT 1291
 412   I   Y   C   Y   C   N   G   E   V   Q   A   E   V   K   K   M   W   S   R   W   431

                    1390              1410              1430
1292 GGAATCTCTCCGTGGACTGGAAAAAGGACACCGGCCATGTGGCAGCCGCAGATGCGGGCTCAG 1351
 432   N   L   S   V   D   W   K   R   T   P   P   C   G   S   R   R   C   G   S   V   451

                    1450              1470              1490
1352 TGCTCACCACCGTGACGCACAGCACCAGCAGCCAGTCACAGGTGGGCGGCAGCACACGCAT 1411
 452   L   T   T   V   T   H   S   T   S   S   Q   S   Q   V   A   A   A   H   A   W   471

                    1510              1530              1550
1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAAGCTGCCAGCAGCAGACAGCCACATCAC 1471
 472   C   L   S   L   A   K   L   P   R   S   P   A   D   S   L   T   A   T   S   L   491
```

FIG.1D

```
                  1570                1590                1610
1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACTCTTCCACGA 1531
 492   Y  L  A  M  S  G  V  T  Q  S  R  T  A  S  H  T  L  S  T  R  511

                  1630                1650                1670
1532 GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA 1591
 512   S  N  K  E  D  S  G  R  Q  R  D  D  I  L  M  E  K  P  S  R  531

                  1690                1710                1730
1592 GGCCTATGGAATCTAACCCAGACACTGAAGGATGACAAGGAGAAACTGAGGATGTTCTCT 1651
 532   P  M  E  S  N  P  D  T  E  G                                541

                  1750                1770                1790
1652 GAATGGACACATGTGTGGCTGACTTTCATGGGCTGGTCCAATGGCTGGTTGTGTGAGAGGGC 1711

                  1810                1830                1850
1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA 1771

                  1870                1890                1910
1772 TAATAGTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG 1831

                  1930                1950                1970
1832 TGTCAATGGGAGTAGTTATTACCTTCTATTGGCATCAAGTTTCCTCTAAATTAATGTAT 1891

                  1990
1892 GGTATTTGCTCTGTGATTGTTCA                                      1914
```
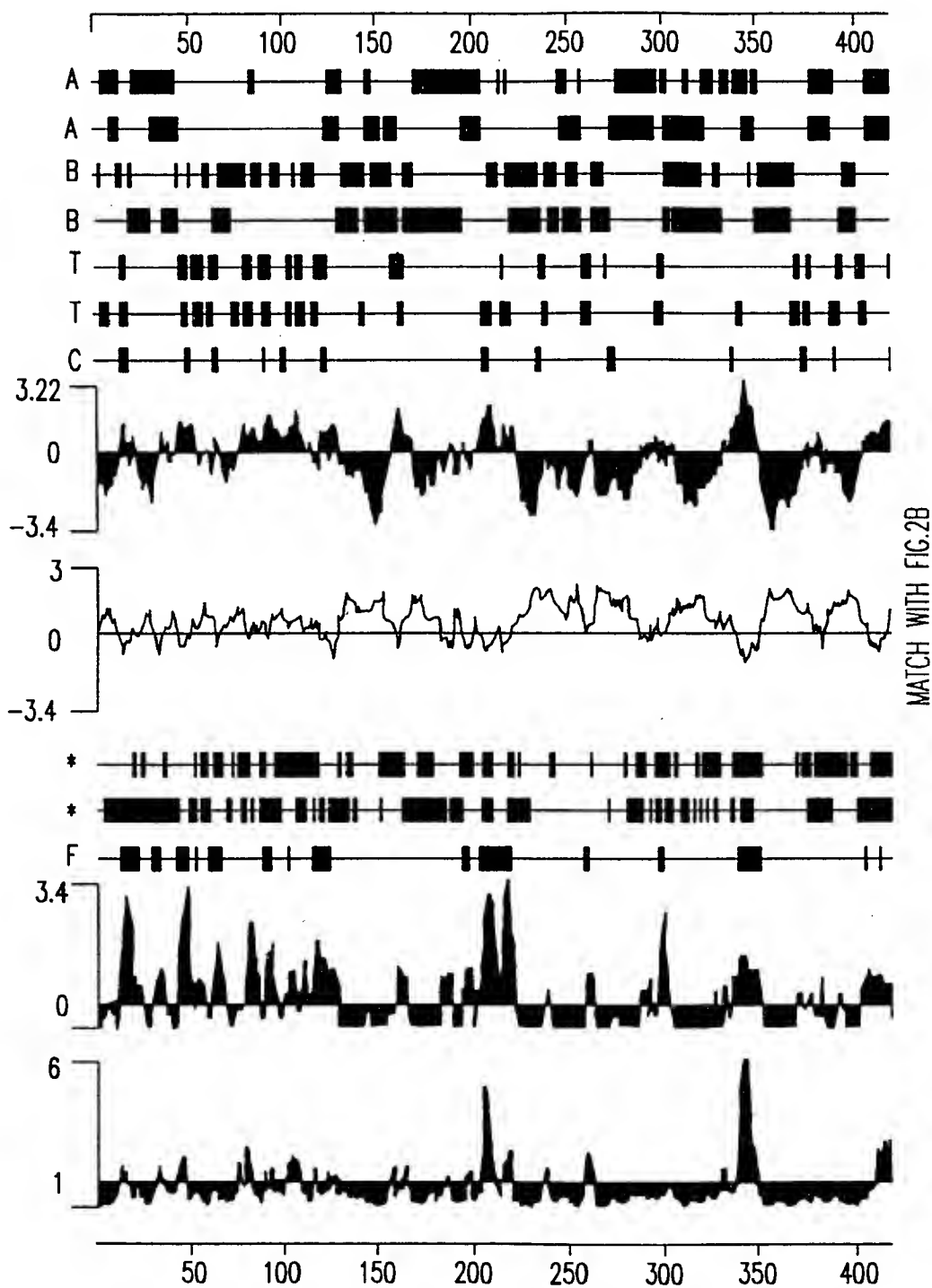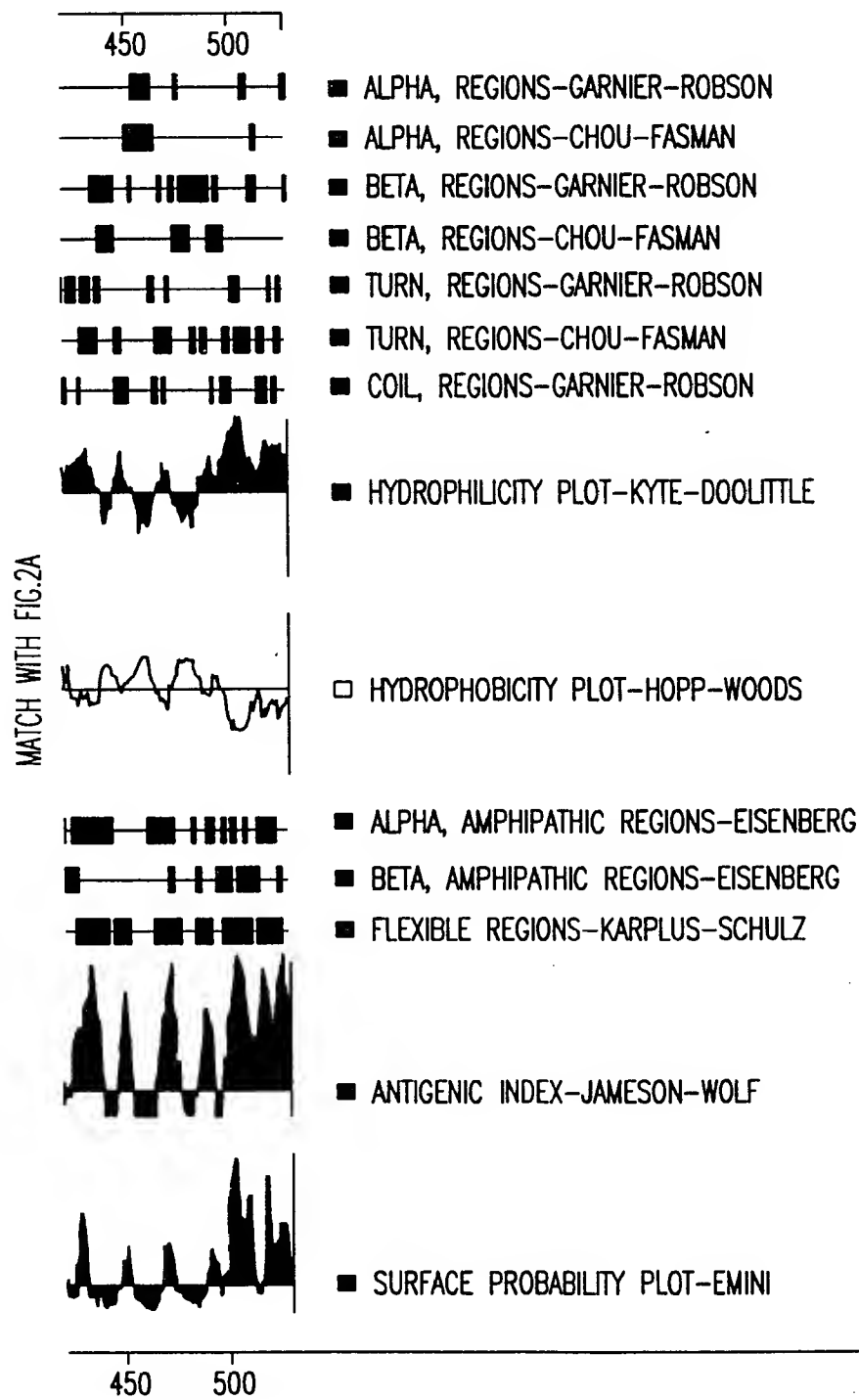
FIG.1E

FIG. 2A

FIG. 2B

TBLASTN 0.95.M9.60

Sequences producing High-scoring Segment Pairs:

		Reading Frame	High Score	Probability P(N)	N
gp|M74445|OPOPTHR_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204	6
pir|S|A39286	parathyroid hormone / parathyroi...	+3	597	2.9e-203	6
gp|L04308|HUMPTHR_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190	5
pir|S|S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189	5
gp|M77184|RATPATHYR_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188	5
gp|X78936|MMPHRPR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188	5
pir|S|A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188	5
gp|L34611|MUSPTHR06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174	5
gp|U11087|HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98	5
gp|M86835|RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the
limiting value of parameter V = 10.

>gp|M74445|OPOPTHR_1 parathyroid hormone receptor [Didelphis virginiana]
        Length = 585

  Plus Strand HSPs:

 Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

                Match with FIG. 3B

                FIG.3A

"PQEFT" GGGGGG

Match with FIG. 3 A

```
Query:  729  IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT  908
             I +++ +  E   DK+ ++GC++AV +F+YFL TNYYWILVEGLYLH+LIF+AFFS+
Sbjct:  253  ITEEELRAFTEPPPADKAGFVGCRVAVTVFLYFLTTNYYWILVEGLYLHSLIFMAFFSEK  312

Query:  909  KYLWGFILIGWGFPAAFVAAWAVARATLADARCWELSAGDIKWIYQAPILAAIGLNFILF  1088
             KYLWGF L GWG PA FVA W   RATLA+  CW+LS+G+ KWI Q PILAAI +NFILF
Sbjct:  313  KYLWGFTLFGWGLPAVFVAWVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF  372

Query:  1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVFGVHYIVFVCLPHS  1244
             +N +RVLATK+ ETNA    DTR+QYRKL KSTLVL+ +FGVHYIVF+  P++
Sbjct:  373  INIIRVLATKLRETNAGRCDTRQQYRKLLKSTLVLMPLFGVHYIVFMATPYT  424
```

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

```
Query:  267  EGNCFPEWDGLICWPRGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTW  446
             +G C PEWD ++CWP G  GK+ AVPCP YIYDFNHKG A+R C+ NG+W+ +  N+TW
Sbjct:  102  DGFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHKGRAYRRCDSNGSWELVPGNNRTW  161

Query:  447  ANYSDCLRFL  476
             ANYS+C++FL
Sbjct:  162  ANYSECVKFL  171
```

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

```
Query:  498  KQEFCERLYVMYTVGYSISFGSLAVAILIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV  677
             ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
```

Match with FIG. 3 C

FIG.3B

MATCH WITH FIG. 3B

```
Sbjct:  177 EREVFDRLGMIYTVGYSISLGSLTVAVLILGYFRRLHCTRNYIHMLFVSFMLRAVSIFI 236

Query:  678 KDRVVHAHIGVKELESLIMQD 740
            KD V+++ +  E+E +   ++
Sbjct:  237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFFNSFQGFFVSIIYCYCNGEVQAEVKKMWSRWNLSVDWKRTPPCGS 1424
            +G+ W+++MH E+ FNSFQGFFV+IIYC+CNGEVQAE+KK WSRW L++D+KR   GS
Sbjct:  427 SGILWQVQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query:  159 AQLDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269
            A +D+D IT EEQI+L+ A+ QCE +  L+  E
Sbjct:   24 ALVDADDVITKEEQIILLRNAQACEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576
            +S + A  A   + H  LPGYV
Sbjct:  512 LSPRLAPGAGASANGHHQLPGYV 534
```

FIG.3C